FIGURE 1

Clone LR4: hLH/CG Receptor Fusion with Thioredoxin Gene in pET32 Vector
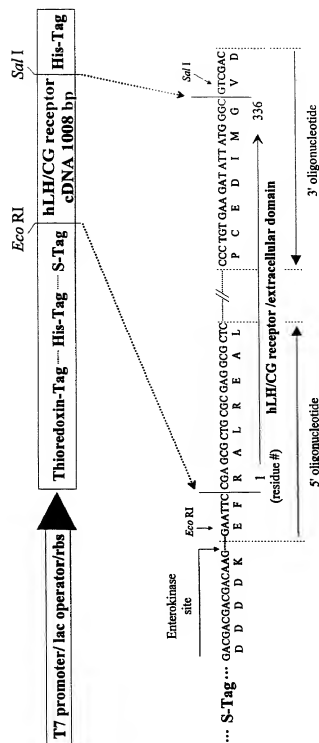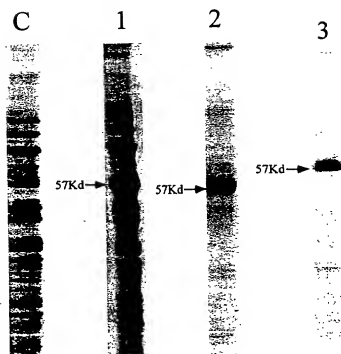
| Thioredoxin-Tag — His-Tag — S-Tag | hLH/CG receptor cDNA 1008 bp | His-Tag |

Eco RI   *Sal* I

T7 promoter/ lac operator/rbs

Enterokinase site

Eco RI   *Sal* I

... S-Tag ... GACGACGACGACAAG—GAATTC CGA GCG CTG CGC GAG GCG CTC // CCC TGT GAA GAT ATT ATG GGC GTCGAC
     D D D D K   E F   R A L R E A L   P C E D I M G V D

                    1   336
        (residue #)

hLH/CG receptor/extracellular domain

5' oligonucleotide   3' oligonucleotide

FIGURE 2

Non-reducing protein gels

Panel A

| C | 1 | 2 | 3 |

57Kd→   57Kd→   57Kd→

Western blots

Murine anti-LHR
polyclonal

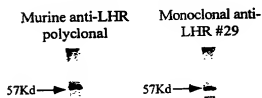Monoclonal anti-
LHR #29

Panel B

57Kd→   57Kd→

FIGURE 3

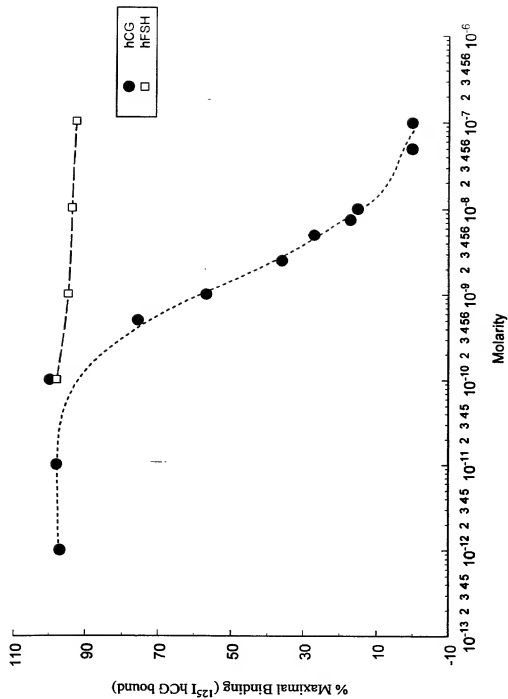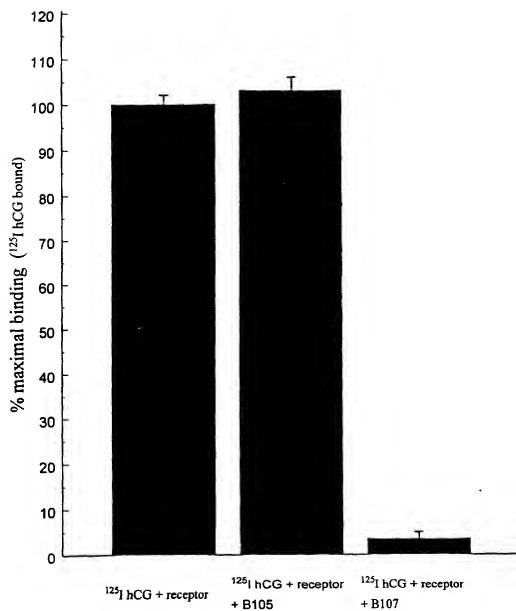Affinity of hLH/CG receptor fusion protein

FIGURE 4

Effect of anti-hCG monoclonal antibodies
on hCG binding to receptor fusion protein

FIGURE 5

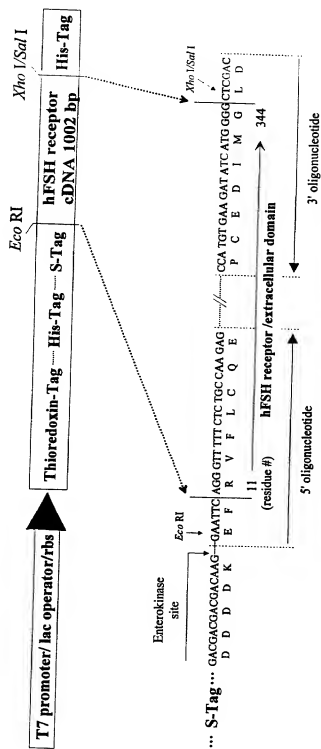hFSH Receptor Fusion with Thioredoxin Gene in pET32 Vector

Figure 6A

```
   1 atgagcgataaaattattcacctgactgac
  31 gacagttttgacacggatgtactcaaagcg
  61 gacggggcgatcctcgtcgatttctgggca
  91 gagtggtgcggtccgtgcaaaatgatcgcc
 121 ccgattctggatgaaatcgctgacgaatat
 151 cagggcaaactgaccgttgcaaaactgaac
 181 atcgatcaaaaccctggcactgcgccgaaa
 211 tatggcatccgtggtatcccgactctgctg
 241 ctgttcaaaaacggtgaagtggcggcaacc
 271 aaagtgggtgcactgtctaaaggtcagttg
 301 aaagagttcctcgacgctaacctggccggt
 331 tctggttctggccatatgcaccatcatcat
 361 catcattcttctggtctggtgccacgcggt
 391 tctggttatgaaagaaaccgctgctgctaaa
 421 ttcgaacgccagcacatggacagcccagat
 451 ctgggtaccgacgacgacgacaaggccatg
 481 gctgatatcggatccgaattcaggggttttt
 511 ctctgccaagagagcaaggtgacagagatt
 541 ccttctgacctcccgaggaatgccattgaa
 571 ctgaggtttgtcctcaccaagcttcgagtc
 601 atccaaaaaggtgcattttcaggatttggg
 631 gacctggagaaaatagagatctctcagaat
 661 gatgtcttggaggtgatagaggcagatgtg
 691 ttctccaaccttcccaaattacatgaaatt
 721 agaattgaaaaggccaacaacctgctctac
 751 atcacccctgaggccttccagaaccttccc
 781 aaccttcaatatctgttaatatccaacaca
 811 ggtattaagcaccttccagatgttcacaag
 841 attcattctctccaaaaggttttacttgac
 871 attcaagataacataaacatccacacaatt
 901 gaaagaaaattctttcgtggggctgagcttt
 931 gaaagtgtgattctatggctgaataagaat
 961 gggattcaagaaatacacaactgtgcattc
 991 aatggaacccaactagatgcagtgaatcta
1021 agcgataataataatttagaagaattgcct
1051 aatgatgttttccacggagcctctggacca
1081 gtcattctagatatttcaagaacaaggatc
1111 cattcctgcctagctatggcttagaaaat
1141 cttaagaagctgagggccaggtcgacttac
1171 aacttaaaaaagctgcctactctggaaaag
1201 cttgtcgccctcatggaagccagcctcacc
1231 tatcccagccattgctgtgcctttgcaaac
1261 tggagacggcaaatctctgagcttcatcca
1291 atttgcaacaaatctattttaaggcaagaa
1321 gttgattatatgactcaggctaggggtcag
1351 agatcctctctggcagaagacaatgagtcc
1381 agctacagcagaggatttgacatgacgtac
1411 actgagtttgactatgtacttatgcaatgaa
1441 gtggttgacgtgacctgctcccctaagcca
1471 gatgcattcaacccatgtgaagatatcatg
1501 ggggtcgacaagcttgcggccgcactcgag
1531 caccaccaccaccaccactga
```

Figure 6B

```
  1 MSDKIIHLTDDSFDTDVLKADGAILVDFWA
 31 EWCGPCKMIAPILDEIADEYQGKLTVAKLN
 61 IDQNPGTAPKYGIRGIPTLLLFKNGEVAAT
 91 KVGALSKGQLKEFLDANLAGSGSGHMHHHH
121 HHSSGLVPRGSGMKETAAAKFERQHMDSPD
151 LGTDDDDKAMADIGSEFRVFLCQESKVTEI
181 PSDLPRNAIELRFVLTKLRVIQKGAFSGFG
211 DLEKIEISQNDVLEVIEADVFSNLPKLHEI
241 RIEKANNLLYITPEAFQNLPNLQYLLISNT
271 GIKHLPDVHKIHSLQKVLLDIQDNINIHTI
301 ERNSFVGLSFESVILWLNKNGIQEIHNCAF
331 NGTQLDAVNLSDNNNLEELPNDVFHGASGP
361 VILDISRTRIHSLPSYGLENLKKLRARSTY
391 NLKKLPTLEKLVALMEASLTYPSHCCAFAN
421 WRRQISELHPICNKSILRQEVDYMTQARGQ
451 RSSLAEDNESSYSRGFDMTYTEFDYDLCNE
481 VVDVTCSPKPDAFNPCEDIMGVDKLAAALE
511 HHHHHH*
```

Figure 7A

```
   1 atgagcgataaaattattcacctgactgac
  31 gacagttttgacacggatgtactcaaagcg
  61 gacggggcgatcctcgtcgatttctgggca
  91 gagtggtgcggtccgtcaaaatgatcgcc
 121 ccgattctggatgaaatcgctgacgaatat
 151 cagggcaaactgaccgttgcaaaactgaac
 181 atcgatcaaaaccctggcactgcgccgaaa
 211 tatggcatccgtggtatcccgactctgctg
 241 ctgttcaaaaacggtgaagtggcggcaacc
 271 aaagtgggtgcactgtctaaaggtcagttg
 301 aaagagttcctcgacgctaacctggccggt
 331 tctggttctggccatatgcaccatcatcat
 361 catcattcttctggtctggtgccacgcggt
 391 tctggtatgaaagaaaccgctgctgctaaa
 421 ttcgaacgccagcacatggacagcccagat
 451 ctgggtaccgacgacgacgacaaggccatg
 481 gctgatatcggatccgaattccgagcgctg
 511 cgcgaggcgctctgccctgagccctgcaac
 541 tgcgtgcccgacggcgccctgcgctgcccc
 571 ggccccacggcccggtctcactcgactatca
 601 cttgcctacctccctgtcaaagtgatccca
 631 tctcaagctttcagaggacttaatgaggtc
 661 ataaaaattgaaatctctcagattgattcc
 691 ctggaaaggatagaagctaatgcctttgac
 721 aacctcctcaatttgtctgaaatactgatc
 751 cagaacaccaaaaatctgagatacattgag
 781 cccggagcatttataaatcttccccgatta
 811 aaatacttgagcatctgtaacacaggcatc
 841 agaaagtttccagatgttacgaaggtcttc
 871 tcctctgaatcaaatttcattctggaaatt
 901 tgtgataacttacacataaccaccatacca
 931 ggaaatgcttttcaagggatgaataatgaa
 961 tctgtaacactcaaactatatggaaatgga
 991 tttgaagaagtacaaagtcatgcattcaat
1021 gggacgacactgacttcactggagctaaag
1051 gaaaacgtacatctggagaagatgcacaat
1081 ggagccttccgtggggccacagggccgaaa
1111 accttggatatttcttccaccaaattgcag
1141 gccctgccgagctatggcctagagtccatt
1171 cagaggctaattgccacgtcatcctattct
1201 ctaaaaaaattgccatcaagagagaaacattt
1231 gtcaatctcctggaggccacgttgacttac
1261 cccagccactgctgtgctttagaaacttg
1291 ccaacaaaagaacagaattttttcacattcc
1321 atttctgaaaacttttccaaacaatgtgaa
1351 agcacagtaaggaaagtgaataacaaaaca
1381 ctttattcttccatgcttgctgagagtgaa
1411 ctgagtggctgggactatgaatatggtttc
1441 tgcttacccaagacaccccgatgtgctcct
1471 gaaccagatgcttttaatccctgtgaagat
1501 attatgggcgtcgacaagcttgcggccgca
1531 ctcgagcaccaccaccaccaccactga
```

Figure 7B

```
  1 M S D K I I H L T D D S F D T D V L K A D G A I L V D F W A
 31 E W C G P C K M I A P I L D E I A D E Y Q G K L T V A K L N
 61 I D Q N P G T A P K Y G I R G I P T L L L F K N G E V A A T
 91 K V G A L S K G Q L K E F L D A N L A G S G S G H M H H H H
121 H H S S G L V P R G S G M K E T A A A K F E R Q H M D S P D
151 L G T D D D D K A M A D I G S E F R A L R E A L C P E P C N
181 C V P D G A L R C P G P T A G L T R L S L A Y L P V K V I P
211 S Q A F R G L N E V I K I E I S Q I D S L E R I E A N A F D
241 N L L N L S E I L I Q N T K N L R Y I E P G A F I N L P R L
271 K Y L S I C N T G I R K F P D V T K V F S S E S N F I L E I
301 C D N L H I T T I P G N A F Q G M N N E S V T L K L Y G N G
331 F E E V Q S H A F N G T T L T S L E L K E N V H L E K M H N
361 G A F R G A T G P K T L D I S S T K L Q A L P S Y G L E S I
391 Q R L I A T S S Y S L K K L P S R E T F V N L L E A T L T Y
421 P S H C C A F R N L P T K E Q N F S H S I S E N F S K Q C E
451 S T V R K V N N K T L Y S S M L A E S E L S G W D Y E Y G F
481 C L P K T P R C A P E P D A F N P C E D I M G V D K L A A A
511 L E H H H H H H *
```